SEQUENCE LISTING

<110> Durfee, Tim
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      Gruissem, Wilhelm
      Jenkins, Susan
      Roe, Judith
      Zambryski, Patricia

<120> Alteration of Plant Meristem Function by Manipulation of the Retinoblastoma-Like Plant RRB Gene

<130> S-92981

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<141> 2000-03-16

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His Met
25                                        ;

taccatttga gttctctcgg aaattttgag gactagctct aatccctgta gttgatttct     1299

tattgcag aa  agt tct gtc tct tga tgg gag cac ttg cga tga agc ttt      1348
            Gln Ser Ser Val Ser     Trp Glu His Leu Arg     Ser Phe
             30                          35

gaa gtt gtt tac aga aac caa acg aat ttt gtc agc aag cat gtc taa       1396
Glu Val Val Tyr Arg Asn Gln Thr Asn Phe Val Ser Lys His Val
 40                  45                  50

cat tgg aag tgg aa  cggtgaaata cattttttcct ctaacttctc ttttatcagt      1450
His Trp Lys Trp Lys
 55

taactgtggt ttcattatga ctaaatcctt ttttcttctt cttatta g cgg gaa gaa    1507
                                                      Arg Glu Glu
                                                       60

gta gag agg ttc tgg ttt gcg ttt att ctc tat tca gtg aag agg ctt      1555
Val Glu Arg Phe Trp Phe Ala Phe Ile Leu Tyr Ser Val Lys Arg Leu
             65                  70                  75

agt gtg aga aaa gaa gcg gat ggt ctg tca gtg tct ggt gat aat gag      1603
Ser Val Arg Lys Glu Ala Asp Gly Leu Ser Val Ser Gly Asp Asn Glu
 80                  85                  90

ttt aat cta tgt cag ata ctg agg gct ctg aag cta aa  gtaagtagtg       1651
Phe Asn Leu Cys Gln Ile Leu Arg Ala Leu Lys Leu Lys
 95                 100                 105

ttcaattctt ccttccttgt cattcttaaa ttcatttgta gtgacgattt cctctttttc    1711

tgtttatagt a ttg tgg att ttt tta aag agt tac ctc agt ttg tgg tca     1761
             Leu Trp Ile Phe Leu Lys Ser Tyr Leu Ser Leu Trp Ser
             110                 115

agg ctg gat ctg tac tgg gtg aac ttt acg gcg cag act ggg aga aca      1809
Arg Leu Asp Leu Tyr Trp Val Asn Phe Thr Ala Gln Thr Gly Arg Thr
120                 125                 130                 135

gac ttc ag  gttttgacta acatctttta aatatacttc tacttctatt             1857
Asp Phe Arg

atatcattgt taaatatgct tctattaact aattttact tacta g gca aag gag       1912
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                                          Ala Lys Glu
                                            140

gtg cag gct aac ttt gtg cat ctt agc ctt cta agc aag tgagtttagc      1961
Val Gln Ala Asn Phe Val His Leu Ser Leu Leu Ser Lys
        145               150


tcccttccta ttttacattt atctttgttt tgtgtaagaa tagttattga catagatttc    2021

atattttgga cctgcaactt agaagcaaat tttcttccta tgcaataatc agaatatggg    2081

cttgcaatat tccttccatt ttaaattaat taagatttag agttacagat ttctggtttt    2141

catgtgatta tattctgtga attgttttaa ggacatgtta aagtatgatg tttttggtac    2201

ctttccttgg taaca gat act aca aac gtg ggt tcc ggg aat tct ttt tga    2252
               Asp Thr Thr Asn Val Gly Ser Gly Asn Ser Phe
                155               160               165

cat atg atg caa acg cag aaa aga act cag caa act ctt cta cct att    2300
His Met Met Gln Thr Gln Lys Arg Thr Gln Gln Thr Leu Leu Pro Ile
            170               175               180

tgc tgg ata gtt atc gtt ttg gat ggc tac tct ttt tgg cac tcc gaa    2348
Cys Trp Ile Val Ile Val Leu Asp Gly Tyr Ser Phe Trp His Ser Glu
            185               190               195

acc atg cgt tta gtc gat tta agg acc tcg tga cat gct caa atg gcg    2396
Thr Met Arg Leu Val Asp Leu Arg Thr Ser     His Ala Gln Met Ala
        200               205                   210

tag ttt cta tat t ggttagtgac tacctgtgga gctctcccta atctttcatt      2449
    Phe Leu Tyr
        215

cattttagtc ttgctgtaca ttattacttg aaagatgctt cgtttaatat aacgcaattg    2509

aagtataggc taactccttt tcatgttatc a gg  cta ttt tga tca tac atg      2560
                                      Trp Leu Phe     Ser Tyr Met
                                                          220

ttc ctt gtc ggt tta gaa att tca gca tcc aag att ctt ctc gct t      2606
Phe Leu Val Gly Leu Glu Ile Ser Ala Ser Lys Ile Leu Leu Ala
            225               230               235

tggtgagtgt ttatcttttc ttctatcccg ataaccatgg caccatagaa tgtttatcat    2666

ctattttcat ttatgtgatg aatctca gt  taa gaa agg tga caa agg tgt aga    2719
                                Cys     Glu Arg     Gln Arg Cys Arg
                                                            240

ctt ggt tgc atc act ttg caa gat ata tga cgc ctc aga aga tga gtt    2767
Leu Gly Cys Ile Thr Leu Gln Asp Ile     Arg Leu Arg Arg     Val
245               250                   255

gag gat agt aat tga caa ggc aaa taa ttt ggt aga aac cat act gaa    2815
Glu Asp Ser Asn     Gln Gly Lys     Phe Gly Arg Asn His Thr Glu
            260               265               270
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gaa aaa gcc atc tcc agc atc tga gtg cca aac tga caa gct aga taa      2863
Glu Lys Ala Ile Ser Ser Ile     Val Pro Asn     Gln Ala Arg
            275                         280


tat tga ccc a ggttggtcta aaatcatttt ccttcttcaa ttaaagaatc           2913
Tyr     Pro
285


atgtgagttc attgaacagt tgcctgattg ttcttcgaat ctatatggtg ttttactgca   2973


ga tgg ctt gac cta ctt tga gga ttt act gga aga gac gtc cat ctc      3020
Arg Trp Leu Asp Leu Leu     Gly Phe Thr Gly Arg Asp Val His Leu
           290                     295                 300


aac tag ctt aat tac act tga aaa gga tta cta tga tgg taa agg cga     3068
Asn     Leu Asn Tyr Thr     Lys Gly Leu Leu     Trp     Arg Arg
                305                         310


act tga tga gag ggt att cat caa tga aga gga tag ctt act tgg atc     3116
Thr         Glu Gly Ile His Gln     Arg Gly     Leu Thr Trp Ile
                315                         320                 325


tgg aag ctt atc tgc agg agc tgt taa tat tac tgg tgt taa gag gaa     3164
Trp Lys Leu Ile Cys Arg Ser Cys     Tyr Tyr Trp Cys     Glu Glu
                    330                     335


aat tga tgc ttt gag ctc acc tgc aag gac att tat aag ccc act ttc     3212
Asn     Cys Phe Glu Leu Thr Cys Lys Asp Ile Tyr Lys Pro Thr Phe
340                         345                 350


tcc tca taa gtc gcc tgc tgc taa gac aaa tgg tat tag cgg tgc tac     3260
Ser Ser     Val Ala Cys Cys     Asp Lys Trp Tyr     Arg Cys Tyr
355                         360                 365


caa gtt ggc agc aac acc agt gag cac agc aat gac aac tgc caa gtg     3308
Gln Val Gly Ser Asn Thr Ser Glu His Ser Asn Asp Asn Cys Gln Val
            370                 375                 380


gct cag gac tgt cat atc ccc gct tct gcc aaa acc ttc tcc tgg gtt     3356
Ala Gln Asp Cys His Ile Pro Ala Ser Ala Lys Thr Phe Ser Trp Val
            385                 390                 395


gga aca ttt cct taa atc atg tga tag gga tat aac aaa tga cgt cac     3404
Gly Thr Phe Pro     Ile Met         Gly Tyr Asn Lys     Arg His
400                     405                             410


acg aag agc aca cat aat att gga agc tat ttt ccc aaa tag ttc cct     3452
Thr Lys Ser Thr His Asn Ile Gly Ser Tyr Phe Pro Lys     Phe Pro
                415                 420                     425


tgg tgc cca atg tgg agg tgg aag ttt gca agc tgt tga cct gat gga     3500
Trp Cys Pro Met Trp Arg Trp Lys Phe Ala Ser Cys     Pro Asp Gly
                430                 435                 440


tga cat atg ggc aga gca gcg cag att aga agc ttg taa gtt ata cta     3548
    His Met Gly Arg Ala Ala Gln Ile Arg Ser Leu     Val Ile Leu
                445                 450                         455


cag agt tct tga ggc aat gtg taa agc aga agc tca gat ttt gca tgc     3596
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                              Page 29

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Gln Ser Ser       Gly Asn Val     Ser Arg Ser Ser Asp Phe Ala Cys
                  460                     465

aaa taa tct gaa ctc ttt att gac aaa tga gag gtt cca tag atg cat      3644
Lys     Ser Glu Leu Phe Ile Asp Lys     Glu Val Pro     Met His
470                     475                     480

gct tgc ttg ctc agc tga att ggt act ggc tac cca caa aac aat tac      3692
Ala Cys Leu Leu Ser     Ile Gly Thr Gly Tyr Pro Gln Asn Asn Tyr
        485                     490      495

aat gtt gtt ccc agc tgt tct gga gag gac tgg gat cac agc ctt tga      3740
Asn Val Val Pro Ser Cys Ser Gly Glu Asp Trp Asp His Ser Leu
        500                     505             510

tct cag caa ggt aat tga gag ttt cat acg aca tga aga ttc tct gcc      3788
Ser Gln Gln Gly Asn     Glu Phe His Thr Thr     Arg Phe Ser Ala
        515                     520                     525

tag aga gtt gag acg aca tct gaa ttc act gga gga acg gct tct aga      3836
    Arg Val Glu Thr Thr Ser Glu Phe Thr Gly Gly Thr Ala Ser Arg
            530                     535                     540

gag tat ggt atg gga gaa agg ctc ttc aat gta caa ttc tct gat tgt      3884
Glu Tyr Gly Met Gly Glu Arg Leu Phe Asn Val Gln Phe Ser Asp Cys
            545                     550                     555

tgc cag gcc atc gct tgc att gga gat aaa tca gct cgg ttt act agc      3932
Cys Gln Ala Ile Ala Cys Ile Gly Asp Lys Ser Ala Arg Phe Thr Ser
        560                     565                     570

tga acc aat gcc atc tct gga tgc aat cgc agc act tat taa ttt ctc      3980
    Thr Asn Ala Ile Ser Gly Cys Asn Arg Ser Thr Tyr     Phe Leu
        575                     580                     585

tga cgg agc aaa tca tgc atc atc tgt aca aaa gca tga aac ttg tcc a   4029
    Arg Ser Lys Ser Cys Ile Ile Cys Thr Lys Ala     Asn Leu Ser
        590                     595                     600

ggtagtttta tttgtttctg aattaaagca gttttccaac ctgctgttaa tggtatgatt  4089

ttcttaccaa aaattgtcaa atttgctgcc atata gg  aca aaa tgg ggg gat     4141
                                        Arg Thr Lys Trp Gly Asp
                                                        605

tag atc gcc caa aag att atg tac tga tta ccg cag cat tct agt tga      4189
    Ile Ala Gln Lys Ile Met Tyr     Leu Pro Gln His Ser Ser
        610                     615                     620

acg caa ttc ctt tac atc acc agt aaa gga tcg tct gtt ggc ctt agg      4237
Thr Gln Phe Leu Tyr Ile Thr Ser Lys Gly Ser Ser Val Gly Leu Arg
        625                     630                     635

caa cgt taa atc caa gat gct gcc acc tcc gtt gca gtc tgc att tgc      4285
Gln Arg     Ile Gln Asp Ala Ala Thr Ser Val Ala Val Cys Ile Cys
        640                     645                     650

ca  ggtacatttt gagtaactat gagtagaaat ggagagttag tttacctatc          4337
Gln
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tagttgtccc tgtacttgtt aagtaacctc ttcggattta tgtctaca g ccc aac   4392
                                                                         Pro Asn

acg gcc caa ccc agg agg tgg agg aga aac ttg tgc aga aac tgg aat   4440
Thr Ala Gln Pro Arg Arg Trp Arg Arg Asn Leu Cys Arg Asn Trp Asn
655   660   665   670

caa tat ttt ctt cac aaa ggtaggtctg tgagatcttt ggatctacta   4488
Gln Tyr Phe Leu His Lys
                 675

ctaatcgttt ggttagatga tgtactacaa aacacggtat tgattcttca ttttcggctg   4548

ggaattgtgt taaatgtggt ggctcttccc a gat taa taa att ggc tgc tgt   4600
                                       Asp   Ile Gly Cys Cys
                                                         680

aag aat caa tgg aat ggt gga aag act aca act ttc aca gca aat aag   4648
Lys Asn Gln Trp Asn Gly Gly Lys Thr Thr Thr Phe Thr Ala Asn Lys
              685   690   695

gga gag tgt gta ttg ttt ctt cca aca tgt act tgc tca gcg gac ttc   4696
Gly Glu Cys Val Leu Phe Leu Pro Thr Cys Thr Cys Ser Ala Asp Phe
            700   705   710

tct ttt att cag tcg aca cat tga cca gat cat tct ctg ttg ctt cta   4744
Ser Phe Ile Gln Ser Thr His   Pro Asp His Ser Leu Leu Leu Leu
             715   720   725

cgg agt ggc caa ggtgagtagt gtgattcaaa gggtttaact atatgtcatc   4796
Arg Ser Gly Gln
             730

tggtttacaa tggcttctct tacacttaca ctttttccat gaatcacctt gtagatatcc   4856

caaatgagcc tga ctt tca ggg aaa tca tat aca act acc gga agc aac   4905
                           Leu Ser Gly Lys Ser Tyr Thr Thr Thr Gly Ser Asn
                                     735   740

cac agt gta aac cat tag ttt tcc gca gcg ttt atg tgg atg cgt tac   4953
His Ser Val Asn His   Phe Ser Ala Ala Phe Met Trp Met Arg Tyr
745   750   755

aat gtc gcc gtc aag g ggtatatata cactcttaac cttatgctga aaagtttctt   5009
Asn Val Ala Val Lys
760

tactcggtgg agaagactaa atttgtgaca atgacttgaa ca ga gaa tag ggc   5062
                                                     Gly Glu   Gly

cag atc atg ttg aca tca tca cat tct aca atg aaa tat tta ttc ctg   5110
Gln Ile Met Leu Thr Ser Ser His Ser Thr Met Lys Tyr Leu Phe Leu
              770   775   780

ccg taa agc cgc tgc tgg tgg agc tag gtc ctg taa gaa acg acc ggg   5158

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Pro      Ser Arg Cys Trp Trp Ser    Val Leu    Glu Thr Thr Gly
         785             790                    795

ctg tgg aag cca ata ata agc ctg aa  ggtagttaag aaaggccaga         5204
Leu Trp Lys Pro Ile Ile Ser Leu Lys
            800

tacttgttag atgtaagctt tgtctatcaa tttagtccct aagttaaatg atcgtcttat  5264

tttggattca ca g gtc aat gtc ccg gat cgc caa agg tgt ctg tgt ttc    5313
              Val Asn Val Pro Asp Arg Gln Arg Cys Leu Cys Phe
                       810               815

caa gtg ttc cag aca tgt ccc cta aaa aag tat ctg cag tgc aca atg    5361
Gln Val Phe Gln Thr Cys Pro Leu Lys Lys Tyr Leu Gln Cys Thr Met
    820             825               830

ttt atg ttt ctc ctc ttc ggg gat caa ag  gtaaagaaga tcatagtgct     5410
Phe Met Phe Leu Leu Phe Gly Asp Gln Arg
    835             840

taactcttta tcatgatatg actaagtctt gaggaggagg taggtgacaa gattgtttgg  5470

ttaccttcca tgtgttgtgt gtttgca g atg gat gct ctt att tca cac agt   5522
                            Met Asp Ala Leu Ile Ser His Ser
                                845               850

aca aag agt tac tat gct tgt gtt gga gag agt aca cat gct tac cag    5570
Thr Lys Ser Tyr Tyr Ala Cys Val Gly Glu Ser Thr His Ala Tyr Gln
        855             860                   865

agc cct tca aag gac cta tct gcc atc aac aac cgc ttg aac a          5613
Ser Pro Ser Lys Asp Leu Ser Ala Ile Asn Asn Arg Leu Asn
        870             875               880

agtaagtaaa aaaatcacgt ctctcatcag cttcttccat aaaaccaatc actgacccaa  5673

tccaatttca tctggtgtca ca gc  agc agc agc aac cgc aag agg acg cta   5724
                          Ser Ser Ser Asn Arg Lys Arg Thr Leu
                              885                   890

aac ttt gac gca gaa gca ggg atg gtc agc gat tcc atg gta gca aat    5772
Asn Phe Asp Ala Glu Ala Gly Met Val Ser Asp Ser Met Val Ala Asn
        895             900               905

agc ctt aac ctc caa aac caa aat caa aac caa aat gga agc gat gca    5820
Ser Leu Asn Leu Gln Asn Gln Asn Gln Asn Gln Asn Gly Ser Asp Ala
        910             915               920

tcg tcc tca ggt ggt gcc gca ccc ctt aaa acc gag cca aca gat tca    5868
Ser Ser Ser Gly Gly Ala Ala Pro Leu Lys Thr Glu Pro Thr Asp Ser
    925             930               935

ta gatatctctc tctacttgct acaccaactt ctcttcagtt atagcatctg          5920

taaatcctta tgttgcagag tttgctttta tgtttagctt ctagtttat agtgatcacc   5980

tcaggctatg agcggatgga tcccttt att gtttctttt tctttttta tcttagttaa   6040
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gtcagtctta ataagcatta ataaatgtct ttttcttgtt cactctttct aactgtgttc    6100

ggtgtcccat ctactaaatt tattttccac tttaaaaaaa aacaatttgt gacatttact    6160

taacttggaa catatacagt acagttaagc aattaactat aaccaacaaa ttgtctgaac    6220

aattgtctgt cttacctttt tagctctcta taaatttacg ccgcaaaaca acactttatg    6280

tcgatttcag aataacttac tactccagca tatttctcaa aactttctca ataggttaaa    6340

tttaaaacaa ccttgcaact tatgaaaaaa tcctccagca aatttgccag aaaagaatgt    6400

tacaatggct acaatcacat cc                                            6422
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